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RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/485,163

DATE: 10/29/97  
TIME: 15:37:02

INPUT SET: S21268.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

- 1  
2  
3 (1) General Information:  
4  
5 (i) APPLICANT: Beaudry, Gary A.  
6 Maddon, Paul J.  
7  
8 (ii) TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMERAS  
9  
10 (iii) NUMBER OF SEQUENCES: 10  
11  
12 (iv) CORRESPONDENCE ADDRESS:  
13 (A) ADDRESSEE: Cooper & Dunham LLP  
14 (B) STREET: 1185 Avenue of the Americas  
15 (C) CITY: New York  
16 (D) STATE: New York  
17 (E) COUNTRY: USA  
18 (F) ZIP: 10036  
19  
20 (v) COMPUTER READABLE FORM:  
21 (A) MEDIUM TYPE: Floppy disk  
22 (B) COMPUTER: IBM PC compatible  
23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
24 (D) SOFTWARE: PatentIn Release #1.24  
25  
26 (vi) CURRENT APPLICATION DATA:  
27 (A) APPLICATION NUMBER: 08/485,163  
28 (B) FILING DATE: 07-JUN-1995  
29 (C) CLASSIFICATION:  
30  
31 (vii) ATTORNEY/AGENT INFORMATION:  
32 (A) NAME: White, John P.  
33 (B) REGISTRATION NUMBER: 28,678  
34 (C) REFERENCE/DOCKET NUMBER: 37690-II-1-PCT-US  
35  
36 (viii) TELECOMMUNICATION INFORMATION:  
37 (A) TELEPHONE: (212) 278-0400  
38 (B) TELEFAX: (212) 391-0525  
39 (C) TELEX:  
40  
41 (2) INFORMATION FOR SEQ ID NO:1:  
42  
43 (i) SEQUENCE CHARACTERISTICS:  
44 (A) LENGTH: 13 amino acids  
45 (B) TYPE: amino acid  
46 (C) STRANDEDNESS: unknown

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47                   (D) TOPOLOGY: unknown  
48  
49                   (ii) MOLECULE TYPE: peptide  
50  
51                   (vi) ORIGINAL SOURCE:  
52                    (A) ORGANISM: homo sapien  
53                    (G) CELL TYPE: lymphocyte  
54  
55  
56  
57                   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
58  
59                   Phe Glu Arg Lys Cys Cys Val Gln Cys Pro Pro Cys Asp  
60                   1   5                                     10  
61  
62                   (2) INFORMATION FOR SEQ ID NO:2:  
63  
64                   (i) SEQUENCE CHARACTERISTICS:  
65                    (A) LENGTH: 1796 base pairs  
66                    (B) TYPE: nucleic acid  
67                    (C) STRANDEDNESS: double  
68                    (D) TOPOLOGY: unknown  
69  
70                   (ii) MOLECULE TYPE: cDNA  
71  
72                   (vi) ORIGINAL SOURCE:  
73                    (A) ORGANISM: Homo sapiens  
74                    (G) CELL TYPE: Lymphocyte  
75  
76  
77  
78                   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:  
79  
80                   CAAGCCCCAGA GCCCTGCCAT TTCTGTGGGC TCAGGGTCCCT ACTGCTCAGC CCCTTCCTCC      60  
81  
82                   CTCGGCAAGG CCACAATGAA CCGGGGAGTC CCTTTTAGGC ACTTGCTTCT GGTGCTGCAA      120  
83  
84                   CTGGCGCTCC TCCCAGCAGC CACTCAGGGA AAGAAAGTGG TGCTGGCAA AAAAGGGGAT      180  
85  
86                   ACAGTGGAAC TGACCTGTAC AGCTTCCCAG AAGAAGAGCA TACAATTCCA CTGGAAAAAC      240  
87  
88                   TCCAACCAGA TAAAGATTCT GGGAAATCAG GGCTCCTTCT TAACTAAAGG TCCATCCAAG      300  
89  
90                   CTGAATGATC GCGCTGACTC AAGAAGAAGC CTTTGGGACC AAGGAAACTT CCCCCCTGATC      360  
91  
92                   ATCAAGAACATC TTAAGATAGA AGACTCAGAT ACTTACATCT GTGAAGTGGA GGACCAGAAG      420  
93  
94                   GAGGAGGTGC AATTGCTAGT GTTCGGATTG ACTGCCAACT CTGACACCCA CCTGCTTCAG      480  
95  
96                   GGGCAGAGCC TGACCCCTGAC CTTGGAGAGC CCCCCCTGGTA GTAGCCCCCTC AGTGCAATGT      540  
97  
98                   AGGAGTCCAA GGGTAAAAA CATACAGGGG GGGAAAGACCC TCTCCGTGTC TCAGCTGGAC      600  
99

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PATENT APPLICATION US/08/485,163DATE: 10/29/97  
TIME: 15:37:06**INPUT SET: S21268.raw**

100	CTCCAGGATA GTGGCACCTG GACATGCACT GTCTTCAGA ACCAGAAGAA GGTGGAGTTC	660
101		
102	AAAATAGACA TCGTGGTGCT AGCTTCAGAG CGCAAATGTT GTGTCGAGTG CCCACCGTGC	720
103		
104	CCAGGTAAGC CAGCCCAGGC CTCGCCCTCC AGCTCAAGGC GGGACAGGTG CCCTAGAGTA	780
105		
106	GCCTGCATCC AGGGACAGGC CCCAGCTGGG TGCTGACACG TCCACCTCCA TCTCTTCCTC	840
107		
108	AGCACCCACCT GTGGCAGGAC CGTCAGTCTT CCTCTTCCCC CCAAAACCCA AGGACACCCT	900
109		
110	CATGATCTCC CGGACCCCTG AGGTCACTGT CGTGGTGGTG GACGTGAGCC ACGAAGACCC	960
111		
112	CGAGGTCCAG TTCAACTGGT ACGTGGACGG CGTGGAGGTG CATAATGCCA AGACAAAGCC	1020
113		
114	ACGGGAGGAG CAGTTCAACA GCACGTTCCG TGTGGTCAGC GTCCTCACCG TTGTGCACCA	1080
115		
116	GGACTGGCTG AACGGCAAGG AGTACAAGTG CAAGGTCTCC AACAAAGGCC TCCCAGCCCC	1140
117		
118	CATCGAGAAA ACCATCTCCA AAACCAAAGG TGGGACCCGC GGGGTATGAG GGCCACATGG	1200
119		
120	ACAGAGGCCG GCTCGGCCCA CCCTCTGCC TGGGAGTGAC CGCTGTGCCA ACCTCTGTCC	1260
121		
122	CTACAGGGCA GCCCCGAGAA CCACAGGTGT ACACCCCTGCC CCCATCCCGG GAGGAGATGA	1320
123		
124	CCAAGAACCA GGTCAGCCTG ACCTGCCTGG TCAAAGGCTT CTACCCCCAGC GACATGCCG	1380
125		
126	TGGAGTGGGA GAGCAATGGG CAGCCGGAGA ACAACTACAA GACCACACCT CCCATGCTGG	1440
127		
128	ACTCCGACGG CTCCTTCTTC CTCTACAGCA AGCTCACCGT GGACAAGAGC AGGTGGCAGC	1500
129		
130	AGGGGAAC TG CTTCTCATGC TCCGTGATGC ATGAGGCTCT GCACAACCAC TACACGCAGA	1560
131		
132	AGAGCCTCTC CCTGTCTCCG GGTAAATGAG TGCCACGGCC GGCAAGCCCC CGCTCCCCAG	1620
133		
134	GCTCTCGGGG TCGCGTGAGG ATGCTTGGCA CGTACCCCGT GTACATACTT CCCAGGCACC	1680
135		
136	CAGCATGGAA ATAAAGCACC CAGCGCTGCC CTGGGCCCCCT GCGAGACTGT GATGGTTCTT	1740
137		
138	TCCGTGGTC AGGCCGAGTC TGAGGCCTGA GTGGCATGAG GGAGGCAGAG TGGGTC	1796
139		
140	(2) INFORMATION FOR SEQ ID NO:3:	
141		
142	(i) SEQUENCE CHARACTERISTICS:	
143	(A) LENGTH: 432 amino acids	
144	(B) TYPE: amino acid	
145	(C) STRANDEDNESS: unknown	
146	(D) TOPOLOGY: unknown	
147		
148	(ii) MOLECULE TYPE: protein	
149		
150	(vi) ORIGINAL SOURCE:	
151	(A) ORGANISM: homo sapien	
152	(G) CELL TYPE: lymphocyte	

140 (2) INFORMATION FOR SEQ ID NO:3:

142 (i) SEQUENCE CHARACTERISTICS:  
143 (A) LENGTH: 432 amino acids  
144 (B) TYPE: amino acid  
145 (C) STRANDEDNESS: unknown  
146 (D) TOPOLOGY: unknown

148 (ii) MOLECULE TYPE: protein

150 (vi) ORIGINAL SOURCE:  
151 (A) ORGANISM: homo sapien  
152 (G) CELL TYPE: lymphocyte

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153  
154  
155  
156 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:  
157  
158 Met Asn Arg Gly Val Pro Phe Arg His Leu Leu Leu Val Leu Gln Leu  
159 1 5 10 15  
160  
161  
162 Ala Leu Leu Pro Ala Ala Thr Gln Gly Lys Lys Val Val Leu Gly Lys  
163 20 25 30  
164  
165  
166 Lys Gly Asp Thr Val Glu Leu Thr Cys Thr Ala Ser Gln Lys Lys Ser  
167 35 40 45  
168  
169  
170 Ile Gln Phe His Trp Lys Asn Ser Asn Gln Ile Lys Ile Leu Gly Asn  
171 50 55 60  
172  
173  
174 Gln Gly Ser Phe Leu Thr Lys Gly Pro Ser Lys Leu Asn Asp Arg Ala  
175 65 70 75 80  
176  
177  
178 Asp Ser Arg Arg Ser Leu Trp Asp Gln Gly Asn Phe Pro Leu Ile Ile  
179 85 90 95  
180  
181  
182  
183 Lys Asn Leu Lys Ile Glu Asp Ser Asp Thr Tyr Ile Cys Glu Val Glu  
184 100 105 110  
185  
186  
187 Asp Gln Lys Glu Glu Val Gln Leu Leu Val Phe Gly Leu Thr Ala Asn  
188 115 120 125  
189  
190  
191 Ser Asp Thr His Leu Leu Gln Gly Gln Ser Leu Thr Leu Thr Leu Glu  
192 130 135 140  
193  
194  
195 Ser Pro Pro Gly Ser Ser Pro Ser Val Gln Cys Arg Ser Pro Arg Gly  
196 145 150 155 160  
197  
198 Lys Asn Ile Gln Gly Gly Lys Thr Leu Ser Val Ser Gln Leu Glu Leu  
199 165 170 175  
200  
201  
202 Gln Asp Ser Gly Thr Trp Thr Cys Thr Val Leu Gln Asn Gln Lys Lys  
203 180 185 190  
204  
205

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206 Val Glu Phe Lys Ile Asp Ile Val Val Leu Ala Phe Glu Arg Lys Cys  
207 195 200 205  
208  
209  
210 Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser  
211 210 215 220  
212  
213  
214 Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg  
215 225 230 235 240  
216 Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro  
217 245 250 255  
218  
219  
220  
221 Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala  
222 260 265 270  
223  
224  
225 Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val  
226 275 280 285  
227  
228  
229 Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Glu Tyr  
230 290 295 300  
231  
232  
233 Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr  
234 305 310 315 320  
235  
236 Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu  
237 325 330 335  
238  
239  
240 Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys  
241 340 345 350  
242  
243  
244 Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser  
245 355 360 365  
246  
247  
248 Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp  
249 370 375 380  
250  
251  
252 Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser  
253 385 390 395 400  
254  
255  
256 Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala  
257 405 410 415  
258

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**SEQUENCE VERIFICATION REPORT  
PATENT APPLICATION US/08/485,163**

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Original Text